```
    GAATTCGGCACGAGGTTTTTTTTTTTTTTTTTCCCCTCTTTTCTTTCTTTTCCTTTTGCC
  1 ---------+---------+---------+---------+---------+---------+ 60

    ATCCGAAAGAGCTGTCAGCCGCCGCCGGGCTGCACCTAAAGGCGTCGGTAGGGGGATAAC
 61 ---------+---------+---------+---------+---------+---------+ 120

    AGTCAGAGACCCTCCTGAAAGCAGGAGACGGGACGGTACCCCTCCGGCTCTGCGGGGCGG
121 ---------+---------+---------+---------+---------+---------+ 180

    CTGCGGCCCCTCCGTTCTTTCCCCCTCCCCGAGAGACACTCTTCCTTTCCCCCCACGAAG
181 ---------+---------+---------+---------+---------+---------+ 240

    ACACAGGGGCAGGAACGCGAGCGCTGCCCCTCCGCCATGGGAGGCCGCTTCCTGCTGACG
241 ---------+---------+---------+---------+---------+---------+ 300

    CTCGCCCTCCTCTCGGCGCTGCTGTGCCGCTGCCAGGTTGACGGCTCCGGGGTGTTCGAG
301 ---------+---------+---------+---------+---------+---------+ 360

    CTGAAGCTGCAGGAGTTTGTCAACAAGAAGGGGCTGCTCAGCAACCGCAACTGCTGCCGG
361 ---------+---------+---------+---------+---------+---------+ 420

    GGGGGCGGCCCCGGAGGCGCCGGGCAGCAGCAGTGCGACTGCAAGACCTTCTTCCGCGTC
421 ---------+---------+---------+---------+---------+---------+ 480

    TGCCTGAAGCACTACCAGGCCAGCGTCTCCCCCGAGCCGCCCTGCACCTACGGCAGCGCC
481 ---------+---------+---------+---------+---------+---------+ 540

    ATCACCCCCGTCCTCGGCGCCAACTCCTTCAGCGTCCCCGACGGCGCGGGCGGCGCCGAC
541 ---------+---------+---------+---------+---------+---------+ 600

    CCCGCCTTCAGCAACCCCATCCGCTTCCCCTTCGGCTTCACCTGGCCCGGCACCTTCTCG
601 ---------+---------+---------+---------+---------+---------+ 660

    CTCATCATCGAGGCTCTGCACACCGACTCCCCCGACGACCTCACCACAGAAAACCCCGAG
661 ---------+---------+---------+---------+---------+---------+ 720

    CGCCTCATCAGCCGCCTGGCCACCCAGAGGCACCTGGCGGTGGGCGAGGAGTGGTCCCAG
721 ---------+---------+---------+---------+---------+---------+ 780

    GACCTGCACAGCAGCGGCCGCACCGACCTCAAGTACTCCTATCGCTTTGTGTGTGATGAG
781 ---------+---------+---------+---------+---------+---------+ 840
```

FIG. 1A1

```
     CACTACTACGGGGAAGGCTGCTCTGTCTTCTGCCGGCCCCGTGACGACCGCTTCGGTCAC
841  ---------+---------+---------+---------+---------+---------+ 900

     TTCACCTGTGGAGAGCGTGGCGAGAAGGTCTGCAACCCAGGCTGGAAGGGCCAGTACTGC
901  ---------+---------+---------+---------+---------+---------+ 960

     ACTGAGCCGATTTGCTTGCCTGGGTGTGACGAGCAGCACGGCTTCTGCGACAAACCTGGG
961  ---------+---------+---------+---------+---------+---------+ 1020

     GAATGCAAGTGCAGAGTGGGTTGGCAGGGGCGGTACTGTGACGAGTGCATCCGATACCCA
1021 ---------+---------+---------+---------+---------+---------+ 1080

     GGCTGCCTGCACGGTACCTGTCAGCAGCCATGGCAGTGCAACTGCCAGGAAGGCTGGGGC
1081 ---------+---------+---------+---------+---------+---------+ 1140

     GGCCTTTTCTGCAACCAGGACCTGAACTACTGCACTCACCACAAGCCATGCAAGAATGGT
1141 ---------+---------+---------+---------+---------+---------+ 1200

     CGGTGTACGTGGTTGTGGCCAGTCCCCTCGATGTGAACAAGAACGGCTGGACCCATGTGT
1201 ---------+---------+---------+---------+---------+---------+ 1260

     GGCTCCAGCTGCGAGATTGAAATCAACGAATGTGATGCCAACCCTTGCAAGAATGGTGGA
1261 ---------+---------+---------+---------+---------+---------+ 1320

     AGCTGCACGGATCTCGAGAACAGCTATTCCTGTACCTGCCCCCCAGGCTTCTATGGTAAA
1321 ---------+---------+---------+---------+---------+---------+ 1380

     AACTGTGAGCTGAGTGCAATGACTTGTGCTGATGGACCGTGCTTCAATGGAGGGCGATGC
1381 ---------+---------+---------+---------+---------+---------+ 1440

     ACTGACAACCCTGATGGTGGATACAGCTGCCGCTGCCCACTGGGTTATTCTGGGTTCAAC
1441 ---------+---------+---------+---------+---------+---------+ 1500

     TGTGAAAAGAAAATCGATTACTGCAGTTCCAGCCCTTGTGCTAATGGAGCCCAGTGCGTT
1501 ---------+---------+---------+---------+---------+---------+ 1560

     GACCTGGGGAACTCCTACATATGCCAGTGCCAGGCTGGCTTCACTGGCAGGCACTGTGAC
1561 ---------+---------+---------+---------+---------+---------+ 1620

     GACAACGTGGACGATTGCGCCTCCTTCCCCTGCGTCAATGGAGGGACCTGTCAGGATGGG
1621 ---------+---------+---------+---------+---------+---------+ 1680
```

FIG. 1A2

```
     GTCAACGACTACTCCTGCACCTGCCCCCGGGATACAACGGGAAGAACTGCAGCACGCCG
1681 ---------+---------+---------+---------+---------+---------+ 1740

     GTGAGCAGATGCGAGCACAACCCCTGCCACAATGGGGCCACCTGCCACGAGAGAAGCAAC
1741 ---------+---------+---------+---------+---------+---------+ 1800

     CGCTACGTGTGCGAGTGCGCTCGGGGCTACGGCGGCCTCAACTGCCAGTTCCTGCTCCCC
1801 ---------+---------+---------+---------+---------+---------+ 1860

     GAGCCACCTCAGGGGCCGGTCATCGTTGACTTCACCGAGAAGTACACAGAGGGCCAGAAC
1861 ---------+---------+---------+---------+---------+---------+ 1920

     AGCCAGTTTCCCTGGATCGCAGTGTGCGCCGGGATTATTCTGGTCCTCATGCTGCTGCTG
1921 ---------+---------+---------+---------+---------+---------+ 1980

     TACCAGTCGGTGTACGTCATATCAGAAGAGAAAGATGAGTGCATCATAGCAACTGAGGTG
2401 ---------+---------+---------+---------+---------+---------+ 2460

     TAAAACAGACGTGACGTGGCAAAGCTTATCGATACCGTCATCAAGCTT
2461 ---------+---------+---------+---------+-------- 2508
```

FIG. 1A3

```
   1 GAATTCGGCACGAGGTTTTTTTTTTTTTTTTTCCCCTCTTTTCTTTCTTTTCCTTTTGCCATCCGAAAG   69
  70 AGCTGTCAGCCGCCGCCGGGCTGCACCTAAAGGCGTCGGTAGGGGGATAACAGTCAGAGACCCTCCTGA  138
 139 AAGCAGGAGACGGGACGGTACCCCTCCGGCTCTGCGGGGCGGCTGCGGCCCCTCCGTTCTTTCCCCCTC  207
 208 CCCGAGAGACACTCTTCCTTTCCCCCCACGAAGACACAGGGGCAGGAACGCGAGCGCTGCCCCTCCGCC  276
 277 ATGGGAGGCCGCTTCCTGCTGACGCTCGCCCTCCTCTCGGCGCTGCTGTGCCGCTGCCAGGTTGACGGC  345
 346 TCCGGGGTGTTCGAGCTGAAGCTGCAGGAGTTTGTCAACAAGAAGGGGCTGCTCAGCAACCGCAACTGC  414
 415 TGCCGGGGGGGCGGCCCCGGAGGCGCCGGGCAGCAGCAGTGCGACTGCAAGACCTTCTTCCGCGTCTGC  483
 484 CTGAAGCACTACCAGGCCAGCGTCTCCCCCGAGCCGCCCTGCACCTACGGCAGCGCCATCACCCCCGTC  552
 553 CTCGGCGCCAACTCCTTCAGCGTCCCCGACGGCGCGGGCGGCGCCGACCCCGCCTTCAGCAACCCCATC  621
 622 CGCTTCCCCTTCGGCTTCACCTGGCCCGGCACCTTCTCGCTCATCATCGAGGCTCTGCACACCGACTCC  690
 691 CCCGACGACCTCACCACAGAAAACCCCGAGCGCCTCATCAGCCGCCTGGCCACCCAGAGGCACCTGGCG  759
 760 GTGGGCGAGGAGTGGTCCCAGGACCTGCACAGCAGCGGCCGCACCGACCTCAAGTACTCCTATCGCTTT  828
 829 GTGTGTGATGAGCACTACTACGGGGAAGGCTGCTCTGTCTTCTGCCGGCCCCGTGACGACCGCTTCGGT  897
 898 CACTTCACCTGTGGAGAGCGTGGCGAGAAGGTCTGCAACCCAGGCTGGAAGGGCCAGTACTGCACTGAG  966
 967 CCGATTTGCTTGCCTGGGTGTGACGAGCAGCACGGCTTCTGCGACAAACCTGGGGAATGCAAGTGCAGA 1035
1036 GTGGGTTGGCAGGGGCGGTACTGTGACGAGTGCATCCGATACCCAGGCTGCCTGCACGGTACCTGTCAG 1104
1105 CAGCCATGGCAGTGCAACTGCCAGGAAGGCTGGGGCGGCCTTTTCTGCAACCAGGACCTGAACTACTGC 1173
1174 ACTCACCACAAGCCATGCAAGAATGGTGCCACATGCACCAACACCGGTCAGGGGAGCTACACTTGTTCT 1242
1243 TGCCGACCTGGGTACACAGGCTCCAGCTGCGAGATTGAAATCAACGAATGTGATGCCAACCCTTGCAAG 1311
1312 AATGGTGGAAGCTGCACGGATCTCGAGAACAGCTATTCCTGTACCTGCCCCCCAGGCTTCTATGGTAAA 1380
1381 AACTGTGAGCTGAGTGCAATGACTTGTGCTGATGGACCGTGCTTCAATGGAGGGCGATGCACTGACAAC 1449
1450 CCTGATGGTGGATACAGCTGCCGCTGCCCACTGGGTTATTCTGGGTTCAACTGTGAAAAGAAAATCGAT 1518
1519 TACTGCAGTTCCAGCCCTTGTGCTAATGGAGCCCAGTGCGTTGACCTGGGGAACTCCTACATATGCCAG 1587
1588 TGCCAGGCTGGCTTCACTGGCAGGCACTGTGACGACAACGTGGACGATTGCGCCTCCTTCCCCTGCGTC 1656
1657 AATGGAGGGACCTGTCAGGATGGGGTCAACGACTACTCCTGCACCTGCCCCCCGGGATACAACGGGAAG 1725
1726 AACTGCAGCACGCCGGTGAGCAGATGCGAGCACAACCCCTGCCACAATGGGGCCACCTGCCACGAGAGA 1794
```

FIG. 1B1

```
1795 AGCAACCGCTACGTGTGCGAGTGCGCTCGGGGCTACGGCGGCCTCAACTGCCAGTTCCTGCTCCCCGAG 1863
1864 CCACCTCAGGGGCCGGTCATCGTTGACTTCACCGAGAAGTACACAGAGGGCCAGAACAGCCAGTTTCCC 1932
1933 TGGATCGCAGTGTGCGCCGGGATTATTCTGGTCCTCATGCTGCTGCTGGGTTGCGCCGCCATCGTCGTC 2001
2002 TGCGTCAGGCTGAAGGTGCAGAAGAGGCACCACCAGCCCGAGGCCTGCAGGAGTGAAACGGAGACCATG 2070
2071 AACAACCTGGCGAACTGCCAGCGCGAGAAGGACATCTCCATCAGCGTCATCGGTGCCACTCAGATTAAA 2139
2140 AACACAAATAAGAAAGTAGACTTTCACAGCGATAACTCCGATAAAAACGGCTACAAAGTTAGATACCCA 2208
2209 TCAGTGGATTACAATTTGGTGCATGAACTCAAGAATGAGGACTCTGTGAAAGAGGAGCATGGCAAATGC 2277
2278 GAAGCCAAGTGTGAAACGTATGATTCAGAGGCAGAAGAGAAAAGCGCAGTACAGCTAAAAAGTAGTGAC 2346
2347 ACTTCTGAAAGAAAACGGCCAGATTCAGTATATTCCACTTCAAAGGACACAAAGTACCAGTCGGTGTAC 2415
2416 GTCATATCAGAAGAGAAAGATGAGTGCATCATAGCAACTGAGGTTAGTATCCCACCTGGCAGTCGGACA 2484
2485 AGTCTTGGTGTGTGATTCCCATCCAGCGCAGGTCAGGGCGGCCAAACCATTCTACCTGCTGCCACAGTC 2553
2554 ATCTGTACCCAATGAAAACTGGCCACCTTCAGTCTGTGGCACTGCAGACGTTGAAAAAACTTGTTGTGG 2622
2623 ATTAACATAAGCTCCAGTGGGGGTTACAGGGACAGCAATTTTTGCAGGCAAGGGTATAACTGTAGTGCA 2691
2692 GTTGTAGCTTACTAACCCTACTGACTCATTCTTTCGTGTGCTTCCTGCAGAGCCTGTTTTTGCTTGGCA 2760
2761 TTGAGGTGAAGTCCTGACCCTCTGCATCCTCATAGTCCTCTGCTTTCTTTTTATTAACCTCTTCTGGTC 2829
2830 TCTGCTTGTGTTTTCTCTCAACAGGTGTAAAACAGACGTGACGTGGCAAAGCTT   2883
```

FIG. 1B2

```
  1 MGGRFLLTLA LLSALLCRCQ VDGSGVFELK LQEFVNKKGL LSNRNCCRGG GPGGAGQQQC
 61 DCKTFFRVCL KHYQASVSPE PPCTYGSAIT PVLGANSFSV PDGAGGADPA FSNPIRFPFG
121 FTWPGTFSLI IEALHTDSPD DLTTENPERL ISRLATQRHL AVGEEWSQDL HSSGRTDLKY
181 SYRFVCDEHY YGEGCSVFCR PRDDRFGHFT CGERGEKVCN PGWKGQYCTE PICLPGCDEQ
241 HGFCDKPGEC KCRVGWQGRY CDECIRYPGC LHGTCQQPWQ CNCQEGWGGL FCNQDLNYCT
301 HHKPCKNGAT CTNTGQGSYT CSCRPGYTGS SCEIEINECD ANPCKNGGSC TDLENSYSCT
361 CPPGFYGKNC ELSAMTCADG PCFNGGRCTD NPDGGYSCRC PLGYSGFNCE KKIDYCSSSP
421 CANGAQCVDL GNSYICQCQA GFTGRHCDDN VDDCASFPCV NGGTCQDGVN DYSCTCPPGY
481 NGKNCSTPVS RCEHNPCHNG ATCHERSNRY VCECARGYGG LNCQFLLPEP PQGPVIVDFT
541 EKYTEGQNSQ FPWIAVCAGI ILVLMLLLGC AAIVVCVRLK VQKRHHQPEA CRSETETMNN
601 LANCQREKDI SISVIGATQI KNTNKKVDFH SDNSDKNGYK VRYPSVDYNL VHELKNEDSV
661 KEEHGKCEAK CETYDSEAEE KSAVQLKSSD TSERKRPDSV YSTSKDTKYQ SVYVISEEKD
721 ECIIATEV
```

FIG. 2

```
C-Delta-1    1 MGGRFLLTLA-LLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGGPGGAGQQQC  60
X-Delta-1    1 MGQQRMLTLL-VLSAVL--CQISCSGLFELRLQEFVNKKGLLGNMNCCRPGSL--ASLQRC  56
Delta        1 --MHWIKCLLTAFICFTVIVQVHSSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLG  59

C-Delta-1   61 DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFGF 121
X-Delta-1   57 ECKTFFRICLKHYQSNVSPEPPCTYGGAVTPVLGTNSFVVPES-SNADPTFSNPIRFPFGF 116
Delta       60 SCKTRFRLCLKHYQATIDTTSQCTYGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPFSF 120

C-Delta-1  122 TWPGTFSLIIEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKYSY 182
X-Delta-1  117 TWPGTFSLIIEAIHADSADDLNTENPERLISRLATQRHLTVGEQWSQDLHSSDRTELKYSY 177
Delta      121 SWPGTFSLIVEAWH-DTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYDF 180

C-Delta-1  183 RFVCDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQHGF 243
X-Delta-1  178 RFVCDEYYYGEGCSDYCRPRDDAFGHFSCGERGEKLCNPGWKGLYCTEPICLPGCDEHHGY 238
Delta      181 RVTCDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIPKCAKGCE--HGH 239
                                      DSL

C-Delta-1  244 CDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKP 304
X-Delta-1  239 CDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKP 299
Delta      240 CDKPNQCVCQLGWKGALCNECVLEPNCIHGTCNKPWTCICNEGWGGLYCNQDLNYCTNHRP 300
               EGF1                            EGF2

C-Delta-1  305 CKNGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDA--NPCKNGGSCTD---LENSYSCT 360
X-Delta-1  300 CENGATCTNTGQGSYTCSCRPGYTGSNCEIEVNECDA--NPCKNGGSCSD---LENSYTCS 355
Delta      301 CKNGGTCFNTGEGLYTCKCAPGYSGDDCENEIYSCDADVNPCQNGGTCIDEPHTKTGYKCH 361
                     EGF3                                  EGF4

C-Delta-1  361 CPPGFYGKNCELSAMTCADGPCFNG-----GRCTDNPDGGYSCRCPLGYSGFNCEKKIDYC 416
X-Delta-1  356 CPPGFYGKNCELSAMTCADGPCFNG-----GRCADNPDGGYICFCPGVYSGFNCEKKIDYC 411
Delta      362 CRNGWSGKMCEEKVLTCSDKPCHQGICRNVRPGLGSKGQGYQCECPIGYSGPNCDLQLDNC 422
                                         EGF5
```

FIG. 3A

```
C·Delta·1 417 SSSPCANGAQCVDLGNSYICQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDYSCTCP 477
X·Delta·1 412 SSNPCANGARCEDLGNSYICQCQEGFSGRNCDDNLDDCTSFPCQNGGTCQDGINDYSCTCP 472
Delta     423 SPNPCINGGSCQPSGK---CICPSGFSGTRCETNIDDCLGHQCENGGTCIDMVNQYRCQCV 480
              ------EGF6------------->< ---------------------EGF7---------

C·Delta·1 478 PGYNGKNCSTPVSRCEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGP---- 534
X·Delta·1 473 PGYIGKNCSMPITKCEHNPCHNGATCHERNNRYVCQCARGYGGNNCQFLLPE--------- 524
Delta     481 PGFHGTHCSSKVDLCLIRPCANGGTCLNLNNDYQCTCRAGFTGKDCSVDIDECSSGPCHNG 541
              -------><------------EGF8------------------><---------------

C·Delta·1 535 --------------------------VIVDFTE--KYTEGQNSQFPW--IAVCAGIILVL 564
X·Delta·1 525 ------------------------EKPVVVDLTE--KYTEGQSGQFPW--IAVCAGIVLVL 557
Delta     542 GTCMNRVNSFECVCANGFRGKQCDEESYDSVTFDAHQYGATTQARADGLANAQVVLIAVFS 602
              ---EGF9------------->

C·Delta·1 565 MLLLGCAAIVVCVRLKVQKRHHQPEACRSETETMNNLANCQREKD--ISISVIGATQIKNT 623
X·Delta·1 558 MLLLGCAAVVVCVRVRVQKRRHQPEACRGESKTMNNLANCQREKD--ISVSFIGTTQIKNT 616
Delta     603 VAMPLVAVIAACVVFCMKRKRKRAQEKDNAEARKQNEQNAVATMHHNGSAVGVALASASMG 663
              --TM----------

C·Delta·1 624 NKKVDFHSD-NSDKNGYKVRYPSVDYNLVHELKNEDSVKEEHGKCEAKCETYDSEAEEKSA 683
X·Delta·1 617 NKKIDFLSESNNEKNGYKPRYPSVDYNLVHELKNEDSPKEERSKCEAKCSSNDSDSEDVNS 677
Delta     664 GKTGSNSGLTFDGGNPNIIKNTWDKSVN-NICASAAAAAAAAAADECLMYGGYVASVADN 723

C·Delta·1 684 -----VQLKSSDTSERK---------RPDSVYSTSKDTKYQSVYVISEEKDECIIATEV 728
X·Delta·1 678 -----VHSK-RDSSERR---------RPDSAYSTSKDTKYQSVYVISDEKDECIIATEV 721
Delta     724 NNANSDFCVAPLQRAKSQKQLNTDPTLMHRGSPAGTSAKGASGGGPGAAEGKRISVLGEGS 784

Delta     785 YCSQRWPSLAAAGVAGACSSQLMAAASAAGTDGTAQQQRSVVCGTPHM 832
```

FIG. 3B

```
C-Delta-1    184 V-CDEHYYGE GCSVFCRPRD DRFGHFTCGE RGEKVCNPGW KGQYC 228
Delta        182 VTCDLNYYGS GCAKFCRPRD DSFGHSTCSE TGEIICLTGW QGDYC 226
Serrate      235 VQCAVTYYNT TCTTFCRPRD DQFGHYACGS EGQKLCLNGW QGVNC 279
C-Serrate-1      VTCAEHYYGF GCNKFCRPRD DFFTHHTCDQ NGNKTCLEGW TGPEC

Apx-1        130 NLCSSNYHGK RCNRYCIAN- AKLHWE-CST HGVRRCSAGW SGEDC 172
Lag-2        120 VTCARNYFGN RCENFCDAHL AKAARKRCDA MGRLRCDIGW MGPHC 166
```

FIG. 4

FIG.5A

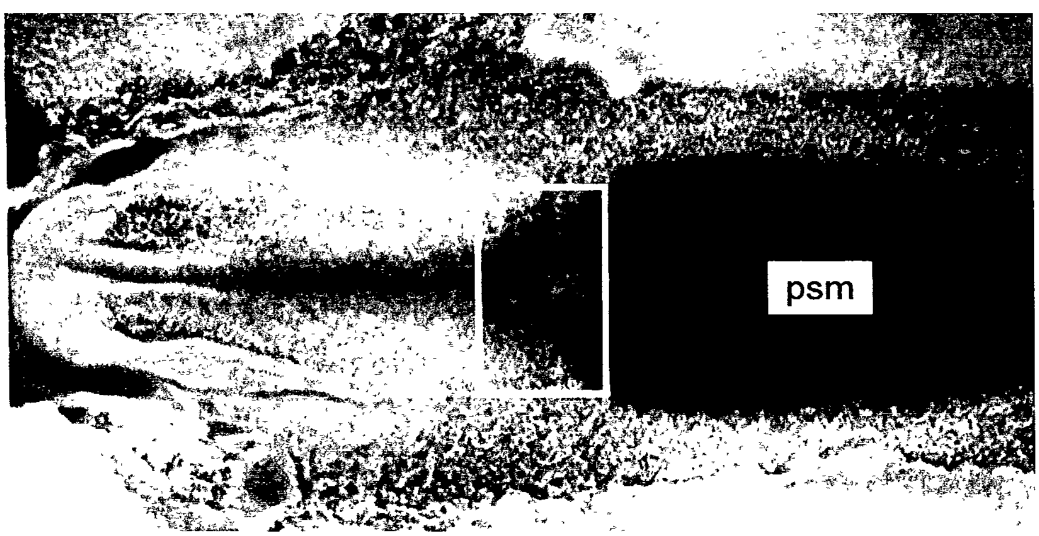


FIG.5B

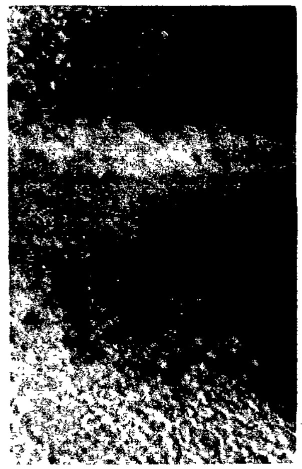

FIG.5C

FIG.5D


FIG.5E

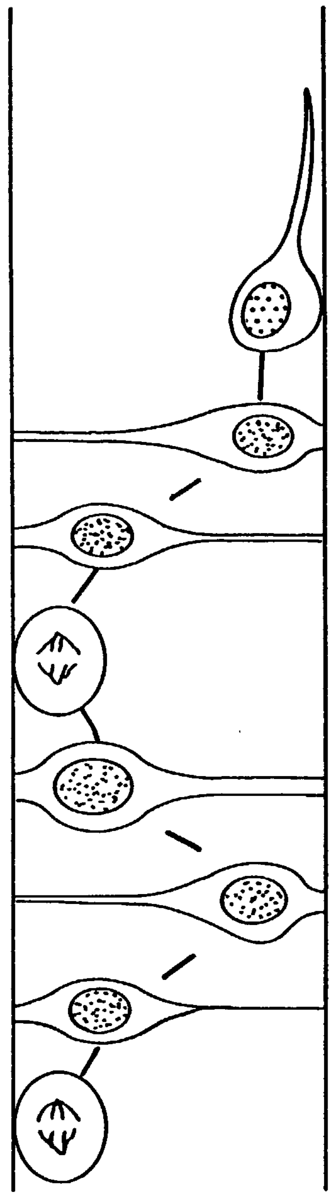


FIG. 6A

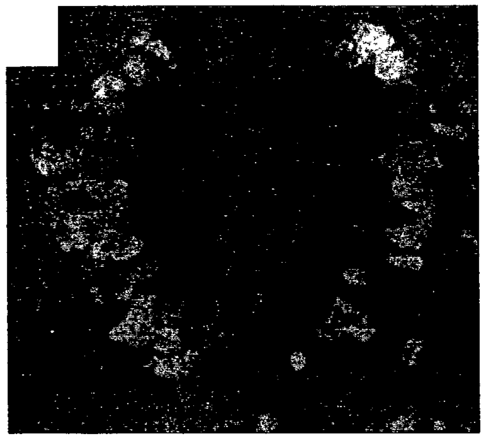

FIG.6B

FIG.6C

```
CTGCAGGAAT TCSMYCGCAT GCTCCCGGCC GCCATGGGCC GTCGGAGCGC GCTAGCCCTT    60
GCCGTGGTCT CTGCCCTGCT GTGCCAGGTC TGGAGCTCCG GCGTATTTGA GCTGAAGCTG   120
CAGGAGTTCG TCAACAAGAA GGGGCTGCTG GGGAACCGCA ACTGCTGCCG CGGGGGCTCT   180
GGCCCGCCTT GCGCCTGCAG GACCTTCTTT CGCGTATGCC TCAAGCACTA CCAGGCCAGC   240
GTGTCACCGG AGCCACCCTG CACCTACGGC AGTGCCGTCA CGCCAGTGCT GGGTGTCGAC   300
TCCTTCAGCC TGCCTGATGG CGCAGGCATC GACCCCGCCT TCAGCAACCC CATCCGATTC   360
CCCTTCGGCT TCACCTGGCC AGGTACCTTC TCTCTGATCA TTGAAGCCCT CCATACAGAC   420
TCTCCCGATG ACCTCGCAAC AGAAAACCCA GAAAGACTCA TCAGCCGCCT GACCACACAG   480
AGGCACCTCA CTGTGGGAGA AGAATGGTCT CAGGACCTTC ACAGTAGCGG CCGCACAGAC   540
CTCCGGTACT CTTACCGGTT TGTGTGTGAC GAGCACTACT ACGGAGAAGG TTGCTCTGTG   600
TTCTGCCGAC CTCGGGATGA CGCCTTTGGC CACTTCACCT GCGGGGACAG AGGGGAGAAG   660
ATGTGCGACC CTGGCTGGAA AGGCCAGTAC TGCACTGACC CAATCTGTCT GCCAGGGTGT   720
GATGACCAAC ATGGATACTG TGACAAACCA GGGGAGTGCA AGTGCAGAGT TGGCTGGCAG   780
GGCCGCTACT GCGATGAGTG CATCCGATAC CCAGGTTGTC TCCATGGCAC CTGCCAGCAA   840
CCCTGGCAGT GTAACTGCCA GGAAGGCTGG GGGGGCCTTT TCTGCAACCA AGACCTGAAC   900
TACTGTACTC ACCATAAGCC GTGCAGGAAT GGAGCCACCT GCACCAACAC GGGCCAGGGG   960
AGCTACACAT GTTCCTGCCG ACCTGGGTAT ACAGGTGCCA ACTGTGAGCT GGAAGTAGAT  1020
GAGTGTGCTC CTAGCCCCTG CAAGAACGGA GCGAGCTGCA CGGACCTTGA GGACAGCTTC  1080
TCTTGCACCT GCCCTCCCGG CTTCTATGGC AAGGTCTGTG AGCTGAGCGC CATGACCTGT  1140
GCAGATGGCC CTTGCTTCAA TGGAGGACGA TGTTCAGATA ACCCTGACGG AGGCTACACC  1200
TGCCATTGCC CCTTGGGCTT CTCTGGCTTC AACTGTGAGA AGAAGATGGA TCTCTGCGGC  1260
TCTTCCCCTT GTTCTAACGG TGCCAAGTGT GTGGACCTCG GCAACTCTTA CCTGTGCCGG  1320
TGCCAGGCTG GCTTCTCCGG GAGGTACTGC GAGGACAATG TGGATGACTG TGCCTCCTCC  1380
```

FIG. 7A

```
CCGTGTGCAA ATGGGGGCAC CTGCCGGGAC AGTGTGAACG ACTTCTCCTG TACCTGCCCA 1440
CCTGGCTACA CGGGCAAGAA CTGCAGCGCC CCTGTCAGCA GGTGTGAGCA TGCACCCTGC 1500
CATAATGGGG CCACCTGCCA CCAGAGGGGC CAGCGCTACA TGTGTGAGTG CGCCCAGGGC 1560
TATGGCGGCC CCAACTGCCA GTTTCTGCTC CCTGAGCCAC CACCAGGGCC CATGGTGGTG 1620
GACCTCAGTG AGAGGCATAT GGAGAGCCAG GGCGGGCCCT TCCCCTGGGT GGCCGTGTGT 1680
GCCGGGGTGG TGCTTGTCCT CCTGCTGCTG CTGGGCTGTG CTGCTGTGGT GGTCTGCGTC 1740
CGGCTGAAGC TACAGAAACA CCAGCCTCCA CCTGAACCCT GTGGGGGAGA GACAGAAACC 1800
ATGAACAACC TAGCCAATTG CCAGCGCGAG AAGGACGTTT CTGTTAGCAT CATTGGGGCT 1860
ACCCAGATCA AGAACACCAA CAAGAAGGCG GACTTTCACG GGGACCATGG AGCCGAGAAG 1920
AGCAGCTTTA AGGTCCGATA CCCCACTGTG GACTATAACC TCGTTCGAGA CCTCAAGGGA 1980
GATGAAGCCA CGGTCAGGGA TACACACAGC AAACGTGACA CCAAGTGCCA GTCACAGAGC 2040
TCTGCAGGAG AAGAGAAGAT CGCCCCAACA CTTAGGGGTG GGGAGATTCC TGACAGAAAA 2100
AGGCCAGAGT CTGTCTACTC TACTTCAAAG GACACCAAGT ACCAGTCGGT GTATGTTCTG 2160
TCTGCAGAAA AGGATGAGTG TGTTATAGCG ACTGAGGTGT AAGATGGAAG CGATGTGGCA 2220
AAATTCCCAT TTCTCTTAAA TAAAATTCCA AGGATATAGC CCCGATGAAT GCTGCTGAGA 2280
GAGGAAGGGA GAGGAAACCC AGGGACTGCT GCTGAGAACC AGGTTCAGGC GAACGTGGTT 2340
CTCTCAGAGT TAGCAGAGGC GCCCGACACT GCCAGCCTAG GCTTTGGCTG CCGCTGGACT 2400
GCCTGCTGGT TGTTCCCATT GCACTATGGA CAGTTGCTTT GAAGAGTATA TATTTAAATG 2460
GACGAGTGAC TTGATTCATA TAGGAAGCAC GCACTGCCCA CACGTCTATC TTGGATTACT 2520
ATGAGCCAGT CTTTCCTTGA ACTAGAAACA CAACTGCCTT TATTGTCCTT TTTGATACTG 2580
AGATGTGTTT TTTTTTTTTC CTAGACGGGA AAAAGAAAAC GTGTGTTATT TTTTTTGGGA 2640
TTTGTAAAAA TATTTTTCAT GATTATGGGA GAGCTCCCAA CGCGTTGGAG GT         2692
```

FIG. 7B

```
MGRRSALALA VVSALLCQVW SSGVFELKLQ EFVNKKGLLG NRNCCRGGSG   50
PPCACRTFFR VCLKHYQASV SPEPPCTYGS AVTPVLGVDS FSLPDGAGID  100
PAFSNPIRFP FGFTWPGTFS LIIEALHTDS PDDLATENPE RLISRLTTQR  150
HLTVGEEWSQ DLHSSGRTDL RYSYRFVCDE HYYGEGCSVF CRPRDDAFGH  200
FTCGDRGEKM CDPGWKGQYC TDPICLPGCD DQHGYCDKPG ECKCRVGWQG  250
RYCDECIRYP GCLHGTCQQP WQCNCQEGWG GLFCNQDLNY CTHHKPCRNG  300
ATCTNTGQGS YTCSCRPGYT GANCELEVDE CAPSPCKNGA SCTDLEDSFS  350
CTCPPGFYGK VCELSAMTCA DGPCFNGGRC SDNPDGGYTC HCPLGFSGFN  400
CEKKMDLCGS SPCSNGAKCV DLGNSYLCRC QAGFSGRYCE DNVDDCASSP  450
CANGGTCRDS VNDFSCTCPP GYTGKNCSAP VSRCEHAPCH NGATCHQRGQ  500
RYMCECAQGY GGPNCQFLLP EPPPGPMVVD LSERHMESQG GPFPWVAVCA  550
GVVLVLLLLL GCAAVVVCVR LKLQKHQPPP EPCGGETETM NNLANCQREK  600
DVSVSIIGAT QIKNTNKKAD FHGDHGAEKS SFKVRYPTVD YNLVRDLKGD  650
EATVRDTHSK RDTKCQSQSS AGEEKIAPTL RGGEIPDRKR PESVYSTSKD  700
TKYQSVYVLS AEKDECVIAT EV                                722
```

FIG. 8

```
CHICK DELTA      MGGRFLLTLA LLSALLCRCQ VDGSGVFELK LQEFVNKKGL LSNRNCCRGG  50
MOUSE DELTA.PEP  MGRRSALALA VVSALLCQ-- VWSSGVFELK LQEFVNKKGL LGNRNCCRGG  48

CONSENSUS        MG.R..L.LA ..SALLC... V..SGVFELD LQEFVNKKGL L.NRNCCRGG  50

CHICK DELTA      GPGGAGQQQC DCKTFFRVCL KHYQASVSPE PPCTYGSAIT PVLGANSFSV 100
MOUSE DELTA.PEP  --SGP---PC ACRTFFRVCL KHYQASVSPE PPCTYGSAVT PVLGVDSFSL  93

CONSENSUS        ...G.....C .C.TFFRVCL KHYQASVSPE PPCTYGSA.T PVLG..SFS. 100

CHICK DELTA      PDGAGGADPA FSNPIRFPFG FTWPGTFSLI IEALHTDSPD DLTTENPERL 150
MOUSE DELTA.PEP  PDGAG-IDPA FSNPIRFPFG FTWPGTFSLI IEALHTDSPD DLATENPERL 142

CONSENSUS        PDGAG..DPA FSNPIRFPFG FTWPGTFSLI IEALHTDSPD DL.TENPERL 150

CHICK DELTA      ISRLATQRHL AVGEEWSQDL HSSGRTDLKY SYRFVCDEHY YGEGCSVFCR 200
MOUSE DELTA.PEP  ISRLTTQRHL TVGEEWSQDL HSSGRTDLRY SYRFVCDEHY YGEGCSVFCR 192

CONSENSUS        ISRL.TQRHL .VGEEWSQDL HSSGRTDL.Y SYRFVCDEHY YGEGCSVFCR 200

CHICK DELTA      PRDDRFGHFT CGERGEKVCN PGWKGQYCTE PICLPGCDEQ HGFCDKPGEC 250
MOUSE DELTA.PEP  PRDDAFGHFT CGDRGEKMCD PGWKGQYCTD PICLPGCDDQ HGYCDKPGEC 242

CONSENSUS        PRDD.FGHFT CG.RGEK.C. PGWKGQYCT. PICLPGCD.Q HG.CDKPGEC 250

CHICK DELTA      KCRVGWQGRY CDECIRYPGC LHGTCQQPWQ CNCQEGWGGL FCNQDLNYCT 300
MOUSE DELTA      KCRVGWQGRY CDECIRYPGC LHFTCQQPWQ CNCQEGWGGL FCNQDLNYCT 292

CONSENSUS        KCRVGWQGRY CDECIRYPGC LHGTCQQPWQ CNCQEGWGGL FCNQDLNYCT 300

CHICK DELTA      HHKPCKNGAT CTNTGQGSTY CSCRPGYTGS SCEIEINECD ANPCKNGGSC 350
MOUSE DELTA.PEP  HHKPCRNGAT CTNTGQGSYT CSCRPGYTGA NCELEVDECA PSPCKNGASC 342

CONSENSUS        HHKPC.NGAT CTNTGQGSYT CSCRPGYTG. .CE.E..EC. ..PCKNG.SC 350

CHICK DELTA      TDLENSYSCT CPPGFYGKNC ELSAMTCADG PCFNGGRCTD NPDGGYSCRC 400
MOUSE DELTA.PEP  TDLEDSFSCT CPPGFYGKVC ELSAMTCADG PCFNGGRCSD NPDGGYTCHC 392

CONSENSUS        TDLE.S.SCT CPPGFYGK.C ELSAMTCADG PCFNGGRC.D NPDGGY.C.C 400

CHICK DELTA      PLGYSGFNCE KKIDYCSSSP CANGAQCVDL GNSYICQCQA GFTGRHCDDN 450
MOUSE DELTA.PEP  PLGFSGFNCE KKMDLCGSSP CSNGAKCVDL GNSYLCRCQA GFSGRYCEDN 442

CONSENSUS        PLG.SGFNCE KK.D.C.SSP C.NGA.CVDL GNSY.C.CQA GF.GR.C.DN 450
```

# FIG.9A

```
CHICK DELTA      VDDCASFPQV NGGTCQDGVN DYSCTCPPGY NGKNCSTPVS RCEHNPCHNG 500
MOUSE DELTA.PEP  VDDCASSPQA NGGTCRDSVN DFSCTCPPGY TGKNCSAPVS RCEHAPCHNG 492

CONSENSUS        VDDCAS.PQ. NGGTC.D.VN D.SCTCPPGY .GKNCS.PVS RCEH.PCHNG 500

CHICK DELTA      ATCHERSNRY VCECARGYGG LNCQFLLPEP PQGPVIVDFT EKYTEGQNSQ 550
MOUSE DELTA      ATCHQRGQRY MCECAQGYGG PNCQFLLPEP PPGPMVVDLS ERHMESQGGP 542

CONSENSUS        ATCH.R..RY .CECA.GYGG .NCQFLLPEP P.GP..VD.. E...E.Q... 550

CHICK DELTA      FPWIAVCAGI ILVLMLLGC AAIVVCVRLK VQKRHHQPEA CRSETETMNN 600
MOUSE DELTA.PEP  FPWVAVCAGV VLVLLLLGC AAVVVCVRLK LQKHQPPPEP CGGETETMNN 592

CONSENSUS        FPW.AVCAG. .LVL.LLGC AA.VVCVRLK .QK....PE. C..ETETMNN 600

CHICK DELTA      LANCQREKDI SISVIGATQI KNTNKKVDFH SDN-SDKNGY KVRYPSVDYN 649
MOUSE DELTA      LANCQREKDV SVSIIGATQI KNTNKKADFH GDHGAEKSSF KVRYPTVDYN 642

CONSENSUS        LANCQREKD. S.S.IGATQI KNTNKK.DFH .D....K... KVRYP.VDYN 650

CHICK DELTA      LVHELKNED- SVKEEHGKCE AKCETYDSEA EEKSAVQLKS SDTSERKRPD 698
MOUSE DELTA.PEP  LVRDLKGDEA TVRDTHSKRD TKCQSQSSAG EEKIAPTLRG GEIPDRKRPE 692

CONSENSUS        LV..LK.... .V...H.K.. .KC....S. EEK.A..L.. .....RKRP. 700

CHICK DELTA      SVYSTSKDTK YQSVYVISEE KDECIIATEV 728
MOUSE DELTA.PEP  SVYSTSKDTK YQSVYVLSAE KDECVIATEV 722
CONSENSUS        SVYSTSKDTK YQSVYV.S.E KDEC.IATEV 730
```

FIG.9B

```
        10         20         30         40         50         60
                    *                     *                     *
TACGATGAAY AACCTGGCGA ACTGCCAGCG TCAGAAGGAC ATCTCAGTCA GCATCATCGG
 Y  D  E   X  P  G  E   L  P  A   *  E  G   H  L  S  Q   H  H  R>
  T  M  N   N  L  A   N  C  Q  R   E  K  D   I  S  V   S  I  I  G>
   R  *  X   T  W  R   T  A  S   V  R  R  T   S  Q  S   A  S  S>

        70         80         90        100        110        120
                    *                     *                     *
GGCYACGTCA GATCARGAAC ACCAACAAGA AGGCGGACTT YMCASCGGGG GACCASAGCG
 G  X  V   R  S  X  T   P  T  R   R  R  T   X  X  R  G   T  X  A>
  A  T  S   D  Q  E   H  Q  Q  E   G  G  L   X  X  G   G  P  X  R>
G  X  R  Q   I  X  N   T  N  K   K  A  D  F   X  X  G   D  X  S>

       130        140        150        160        170        180
                    *                     *                     *
TCCGACAAGA ATGGMTTTCA AGGCCYGCTA CCCCAGCGTG GACTATAACT CGTGCAGGAC
 S  D  K   N  G  F  Q   G  P  L   P  Q  R   G  L  *  L   V  Q  D>
  P  T  R   M  X  F   K  A  R  Y   P  S  V   D  Y  N   S  C  R  T>
V  R  Q  E   W  X  S   R  P  A   T  P  A  W   T  I  T   R  A  G>

       190        200        210        220        230        240
                    *                     *                     *
CTCAAGGGTG ACGACACCGC CGTCAGGACG TCGCACAGCA AGCGTGACAC CAAGTGCCAG
 L  K  G   D  D  T  A   V  R  T   S  H  S   K  R  D  T   K  C  Q>
  S  R  V   T  T  P   P  S  G  R   R  T  A   S  V  T   P  S  A  S>
P  Q  G  *   R  H  R   R  Q  D   V  A  Q  Q   A  *  H   Q  V  P>

       250        260        270        280        290        300
                    *                     *                     *
TCCCCAGGCT CCTCAGGGAG GAGAAGGGGA CCCCGACCAC ACTCAGGGGK TGCGTGCTGC
 S  P  G   S  S  G  R   R  R  G   P  R  P   H  S  G  X   A  C  C>
  P  Q  A   P  Q  G   G  E  G  D   P  D  H   T  Q  G   X  R  A  A>
V  P  R  L   L  R  E   E  K  G   T  P  T  T   L  R  G   C  V  L>

       310        320        330        340        350        360
                    *                     *                     *
GGGCCGGGCT CAGGAGGGGG TACCTGGGGG GTGTCTTCCT GGAACCACTG CTCCGTTTCT
 G  P  G   S  G  G  G   T  W  G   V  S  S   W  N  H  C   S  V  S>
  G  R  A   Q  E  G   V  P  G  G   C  L  P   G  T  T   A  P  F  L>
R  A  G  L   R  R  G   Y  L  G   G  V  F  L   E  P  L   L  R  F>
```

FIG. 10A

```
        370       380       390       400       410       420
                    *                   *                   *
CTTCCCAAAT GTTCTCATGC ATTCATTGTG GATTTTCTCT ATTTTCCTTT TAGTGGAGAA
 L  P  K   C  S  H  A   F  I  V   D  F  L   Y  F  P  F   S  G  E>
  F  P  N   V  L  M   H  S  L  W   I  F  S   I  F  L   L  V  E  K>
S  S  Q  M  F  S  C   I  H  C   G  F  S  L   F  S  F   *  W  R>

       430       440       450       460       470       480
                    *                   *                   *
GCATCTGAAA GAAAAAGGCC GGACTCGGGC TGTTCAACTT CAAAAGACAC CAAGTACCAG
 A  S  E   R  K  R  P   D  S  G   C  S  T   S  K  D  T   K  Y  Q>
  H  L  K   E  K  G   R  T  R  A   V  Q  L   Q  K  T   P  S  T  S>
S  I  *  K   K  K  A   G  L  G  L   F  N  F   K  R  H   Q  V  P>

       490       500       510       520
                    *                   *
TCGGTGTACG TCATATCCGA GGAGAAGGAC GAGTGCGTCA TCGCA
 S  V  Y   V  I  S  E   E  K  D   E  C  V   I  A>
  R  C  T   S  Y  P   R  R  R  T   S  A  S   S>
V  G  V  R   H  I  R   G  E  G   R  V  R  H   R>
```

FIG. 10B

```
   1 TMNNLANCQREKDISVSIIGATQIXNTNKKADFXXGDXSSDKNGFQKARY  50
     |||||||||||||||:|:||||||||||||.|| ::   |||||: |.||
 597 TMNNLANCQREKDISISVIGATQIKNTNKKVDFHSDN..SDKNGY.KVRY 643

  51 PSVDYNLVQDLKGDDTAVRTSHSKRDTKCQSPGSSGRRRGPRPHSGXACC 100
     ||||||||::||.:| .|:..|:| :.||: .:|.:  :::
 644 PSVDYNLVHELKNED.SVKEEHGKCEAKCETYDSEAEEKSA........  683

 101 GPGSGGGTWGVSSWNHCSVSLPKCSHAFIVDFLYFPFSGEASERKRPDSG 150
                                  |::     |::.||||||||.
 684 .............................VQLK....SSDTSERKRPDSV 700

 151 CSTSKDTKYQSVYVISEEKDECVIA  175
     :|||||||||||||||||||||:||
 701 YSTSKDTKYQSVYVISEEKDECIIA  725
```

FIG. 11

```
        10         20         30         40         50         60
     *    *     *    *     *    *     *    *     *    *     *    *
CATTGGGTAC GGGCCCCCCT CGAGGTCGAC GGTATCGATA AGCTTGATAT CGAATTCCGG
        70         80         90        100        110        120
     *    *     *    *     *    *     *    *     *    *     *    *
CTTCACCTGG CCGGGCACCT TCTCTCTGAT TATTGAAGCT CTCCACACAG ATTCTCCTGA
       130        140        150        160        170        180
     *    *     *    *     *    *     *    *     *    *     *    *
TGACCTCGCA ACAGAAAACC CAGAAAGACT CATCAGCCGC CTGGCCACCC AGAGGCACCT
       190        200        210        220        230        240
     *    *     *    *     *    *     *    *     *    *     *    *
GACGGTGGGC GAGGAGTGGT CCCAGGACCT GCACAGCAGC GGCCGCACGG ACCTCAAGTA
       250        260        270        280        290        300
     *    *     *    *     *    *     *    *     *    *     *    *
CTCCTACCGC TTCGTGTGTC ACCAACACTA CTACGGAGAG GGCTGCTCCG TTTTCTGCCG
       310        320        330        340        350        360
     *    *     *    *     *    *     *    *     *    *     *    *
TCCCCGGGAC GATGCCTTCG GCCACTTCAC CTGTGGGGAG CGTGGGGAGA AAGTGTGCAA
       370        380        390        400        410        420
     *    *     *    *     *    *     *    *     *    *     *    *
CCCTGGCTCG AAAGGGCCCT ACTGCACAGA GCCGATCTGC CTGCCTGGAT GTGATGAGCA
       430        440        450        460        470        480
     *    *     *    *     *    *     *    *     *    *     *    *
GCATGGATTT TGTGACAAAC CAGGGGAATG CAAGTGCAGA GTGGGCTGGC AGGGCCGGTA
       490        500        510        520        530        540
     *    *     *    *     *    *     *    *     *    *     *    *
GTGTGACGAG TGTATCCGCT ATCCAGGCTG TCTCCATGGC ACCTGCCAGC AGCCCTGGCA
       550        560        570        580        590        600
     *    *     *    *     *    *     *    *     *    *     *    *
GTGCAACTGC CAGGAAGGNT GGGGGGGCCT TTTCTGCAAC CAGGACCTGA ACTACTGCAC
       610        620        630        640        650        660
     *    *     *    *     *    *     *    *     *    *     *    *
ACACCATAAG CCCTGCAAGA ATGGAGCCAC CTGCAACAAA CACGGGCCAG GGGGAGCTAC
       670        680        690        700        710        720
     *    *     *    *     *    *     *    *     *    *     *    *
ACTTGGTCTT TGGCCGGNCT GGGGTACANA GGGTGCCACC TGCGAAGCTT GGGGATTGGA
       730        740        750        760        770        780
     *    *     *    *     *    *     *    *     *    *     *    *
CGAGTTGTTG ACCCCAGCCC TTGGTAAGAA CGGAGGGAGC TTGACGGATC TTCGGAGAAC
       790        800        810        820        830        840
     *    *     *    *     *    *     *    *     *    *     *    *
AGCTACTCCT GTACCTGCCC ACCCGGCTTC TACGGCAAAA TCTGTGAATT GAGTGCCATG
       850        860        870        880        890        900
     *    *     *    *     *    *     *    *     *    *     *    *
ACCTGTGCGG ACGGCCCTTG CTTTAACGGG GGTCGGTGCT CAGACAGCCC CGATGGAGGG
```

FIG. 12A1

```
       910        920        930        940        950        960
         *         *         *         *         *         *
TACAGCTGCC GCTGCCCCGT GGGCTACTCC GGCTTCAACT GTGAGAAGAA AATTGACTAC
       970        980        990       1000       1010       1020
         *         *         *         *         *         *
TGCAGCTCTT CACCCTGTTC TAATGGTGCC AAGTGTGTGG ACCTCGGTGA TGCCTACCTG
      1030       1040       1050       1060       1070       1080
         *         *         *         *         *         *
TGCCGCTGCC AGGCCGGCTT CTCGGGGAGG CACTGTGACG ACAACGTGGA CGACTGCGCC
      1090       1100       1110       1120       1130       1140
         *         *         *         *         *         *
TCCTCCCCGT GCGCCAACGG ACCTCGGTGA CGGGATGGCG TGAACGACTT CTCCTGCACC
      1150       1160       1170       1180       1190       1200
         *         *         *         *         *         *
TGCCCGCCTG GCTACACGGG CAGGAACTGC AGTGCCCCCG CCAGCACCTG CGAGCACGCA
      1210       1220       1230       1240       1250       1260
         *         *         *         *         *         *
CCCTGCCACA ATGGGGCCAC CTGCCACGAG AGGGGCCACC GCTATNTGTG CGAGCACGCA
      1270       1280       1290       1300       1310       1320
         *         *         *         *         *         *
CGAAGCTACG GGGGTCCCAA CTCCCANTTC CTGCTCCCCC AAACTGCCCC CCCGGCCCCA
      1330       1340       1350       1360       1370       1380
         *         *         *         *         *         *
CGGTGGTGGA AACTCCCCTA AAAAAACCTA AAAGGGCCGG GGGGGGCCCA TCCCCTTGGT
      1390       1400       1410       1420       1430       1440
         *         *         *         *         *         *
GGACGTGTGC GCCGGGGTCA TCCTTGTCCT CATGCTGCTG CTGGGCTGTG CCGCTGTGGT
      1450       1460       1470       1480       1490       1500
         *         *         *         *         *         *
GGTCTGCGTC CGGCTGAGGC TGCAGAAGCA CCGGCCCCCA GCCGACCCCT GNCGGGGGGA
      1510       1520       1530       1540       1550       1560
         *         *         *         *         *         *
GACGGAGACC ATGAACAACC TGGNCAACTG CCAGCGTGAG AAGGACATCT CAGTCAGCAT
      1570       1580       1590       1600       1610       1620
         *         *         *         *         *         *
CATCGGGGNC ACGCAGATCA AGAACACCAA CAAGAAGGCG GACTTCCACG GGGACCACAG
      1630       1640       1650       1660       1670       1680
         *         *         *         *         *         *
NGCCGACAAG AATGGCTTCA AGGCCCGCTA CCCAGNGGTG GACTATAACC TCGTGCAGGA
      1690       1700       1710       1720       1730       1740
         *         *         *         *         *         *
CCTCAAGGGT GACGACACCG CCGTCAGCCA CGCGCACAGC AAGCGTGACA CCAAGTGNCA
      1750       1760       1770       1780       1790       1800
         *         *         *         *         *         *
GCCCCAGGGC TCCTCAGGGG AGGAGAAGGG GACCCCCGAC CCACACTCAG GGGGTGGAGG
```

FIG.12A2

```
       1810       1820       1830       1840       1850       1860
   *    *    *    *    *    *    *    *    *    *    *    *
AAGCATCTTG AAAGAAAAAG GCCGGACTTC GGGCTTGTTC AACTTTCAAA AGACAANCAA
       1870       1880       1890       1900       1910       1920
   *    *    *    *    *    *    *    *    *    *    *    *
NGTACAAGTC GGTGTNCGTC ATTTCCGNAG GAGGAAGGNT GACTGCGTCA TAGGAANTTG
       1930       1940       1950       1960       1970       1980
   *    *    *    *    *    *    *    *    *    *    *    *
AGGTNGTAAA NTGGNAGTTG ANNTTGGAAA GNNNTCCCCG GATTCCGNTT TCAAAGTTTT

T
```

FIG. 12A3

```
        10         20         30         40         50         60
         *    *     *    *     *    *     *    *     *    *     *    *  a.a.no.
CATTGGGTAC GGGCCCCCCT CGAGGTCGAC GGTATCGATA AGCTTGATAT CGAATTCCGG
 H  W  V   R  A  P  L   E  V  D   G  I  D   K  L  D  I   E  F  R>   20
  I  G  Y   G  P  P   S  R  S  T   V  S  I   S  L  I   S  N  S [G>]  20
   L  G  T   G  P  P   R  G  R   R  Y  R  *   A  *  Y   R  I  P>    19

        70         80         90        100        110        120
         *    *     *    *     *    *     *    *     *    *     *    *
CTTCACCTGG CCGGGCACCT TCTCTCTGAT TATTGAAGCT CTCCACACAG ATTCTCCTGA
 L  H  L   A  G  H  L   L  S  D   Y  *  S   S  P  H  R   F  S  *>   40
[ F  T  W   P  G  T   F  S  L  I   I  E  A   L  H  T   D  S  P  D>]  40
A  S  P  G   R  A  P   S  L  *   L  L  K  L   S  T  Q   I  L  L>    39

       130        140        150        160        170        180
         *    *     *    *     *    *     *    *     *    *     *    *
TGACCTCGCA ACAGAAAACC CAGAAAGACT CATCAGCCGC CTGGCCACCC AGAGGCACCT
 *  P  R   N  R  K  P   R  K  T   H  Q  P   P  G  H  P   E  A  P>   60
[ D  L  A   T  E  N   P  E  R  L   I  S  R   L  A  T   Q  R  H  L>]  60
M  T  S  Q   Q  K  T   Q  K  D   S  S  A  A   W  P  P   R  G  T>    59

       190        200        210        220        230        240
         *    *     *    *     *    *     *    *     *    *     *    *
GACGGTGGGC GAGGAGTGGT CCCAGGACCT GCACAGCAGC GGCCGCACGG ACCTCAAGTA
 D  G  G   R  G  V  V   P  G  P   A  Q  Q   R  P  H  G   P  Q  V>   80
[ T  V  G   E  E  W   S  Q  D  L   H  S  S   G  R  T   D  L  K  Y>]  80
*  R  W  A   R  S  G   P  R  T   C  T  A  A   A  A  R   T  S  S>    79

       250        260        270        280        290        300
         *    *     *    *     *    *     *    *     *    *     *    *
CTCCTACCGC TTCGTGTGTG ACGAACACTA CTACGGAGAG GGCTGCTCCG TTTTCTGCCG
 L  L  P   L  R  V  *   R  T  L   L  R  R   G  L  L  R   F  L  P>  100
[ S  Y  R   F  V  C   D  E  H  Y   Y  G  E   G  C  S   V  F  C  R>] 100
T  P  T  A   S  C  V   T  N  T   T  T  E  R   A  A  P   F  S  A>    99

       310        320        330        340        350        360
         *    *     *    *     *    *     *    *     *    *     *    *
TCCCCGGGAC GATGCCTTCG GCCACTTCAC CTGTGGGGAG CGTGGGGAGA AAGTGTGCAA
 S  P  G   R  C  L  R   P  L  H   L  W  G   A  W  G  E   S  V  Q>  120
[ P  R  D   D  A  F   G  H  F  T   C  G  E   R  G  E   K  V  C  N>] 120
V  P  G  T   M  P  S   A  T  S   P  V  C  S   V  G  R   K  C  A>   119
```

FIG.12B1

```
       370        380        390        400        410        420
    *   *     *   *      *   *     *   *     *   *     *   *
CCCTGGCTGG AAAGGGCCCT ACTGCACAGA GCCGATCTGC CTGCCTGGAT GTGATGAGCA
 P  W  L   E  R  A  L   L  H  R   A  D  L   P  A  W  M   *  *  A>   140
 P  G  W   K  G  P   Y  C  T  E   P  I  C   L  P  G   C  D  E  Q>   140
T  L  A  G   K  G  P   T  A  Q   S  R  S  A   C  L  D   V  M  S>    139

       430        440        450        460        470        480
    *   *     *   *      *   *     *   *     *   *     *   *
GCATGGATTT TGTGACAAAC CAGCCCAATG CAAGTGCAGA GTGGGCTGGC AGGGCCGGTA
 A  W  I   L  *  Q  T   R  G  M   Q  V  Q   S  G  L  A   G  P  V>   160
 H  G  F   C  D  K   P  G  E  C   K  C  R   V  G  W  Q   G  R  Y>   160
S  M  D  F   V  T  N   Q  G  N   A  S  A  E   W  A  G   R  A  G>    159

       490        500        510        520        530        540
    *   *     *   *      *   *     *   *     *   *     *   *
CTGTGACGAG TGTATCCGCT ATCCAGGCTG TCTCCATGGC ACCTGCCAGC AGCCCTGGCA
 L  *  R   V  Y  P  L   S  R  L   S  P  W   H  L  P  A   A  L  A>   180
 C  D  E   C  I  R   Y  P  G  C   L  H  G   T  C  Q   Q  P  W  Q>   180
T  V  T  S   V  S  A   I  Q  A   V  S  M  A   P  A  S   S  P  G>    179

       550        560        570        580        590        600
    *   *     *   *      *   *     *   *     *   *     *   *
GTGCAACTGC CAGGAAGGNT GGGGGGGCCT TTTCTGCAAC CAGGACCTGA ACTACTGCAC
 V  Q  L   P  G  R  X   G  G  P   F  L  Q   P  G  P  E   L  L  H>   200
 C  N  C   Q  E  G   W  G  G  L   F  C  N   Q  D  L   N  Y  C  T>   200
S  A  T  A   R  K  X   G  G  A   F  S  A  T   R  T  *   T  T  A>    199

       610        620        630        640        650        660
    *   *     *   *      *   *     *   *     *   *     *   *
ACACCATAAG CCCTGCAAGA ATCGAGCCAC CTGCAACAAA CACGGGCCAG GGGGAGCTAC
 T  P  *   A  L  Q  E   W  S  H   L  Q  Q   T  R  A  R   G  S  Y>   220
 H  H  K   P  C  K   N  G  A  T   C  N  K   H  G  P   G  G  A  T>   220
H  T  I  S   P  A  R   M  E  P   P  A  T   N  T  G  Q   G  E  L>    219

       670        680        690        700        710        720
    *   *     *   *      *   *     *   *     *   *     *   *
ACTTGGTCTT TGGCCGGNCT GGGGTACANA GGGTGCCACC TGCGAAGCTT GGGGATTGGA
 T  W  S   L  A  G  L   G  Y  X   G  C  H   L  R  S  L   G  I  G>   240
 L  G  L   W  P  X   W  G  T  X   G  A  T   C  E  A   W  G  L  D>   240
H  L  V  F   G  R  X   C  V  X   R  V  P  P   A  K  L   G  D  W>    239
```

FIG.12B2

```
      730        740        750        760        770        780
       *    *     *    *     *    *     *    *     *    *     *    *
CGAGTTGTTG ACCCCAGCCC TTGGTAAGAA CGGAGGGAGC TTGACGGATC TTCGGAGAAC
 R  V  V  D  P  S  P  W  *  E  R  R  E  L  D  G  S  S  E  N>    260
  E  L  L  T  P  A  L  G  K  N  G  G  S  L  T  D  L  R  R  T>   260
T  S  C  *  P  Q  P  L  V  R  T  E  Q  A  *  R  I  F  G  E>     259

      790        800        810        820        830        840
       *    *     *    *     *    *     *    *     *    *     *    *
AGCTACTCCT GTACCTGCCC ACCCGGCTTC TACGGCAAAA TCTGTGAATT GAGTGCCATG
 S  Y  S  C  T  C  P  P  G  F  Y  G  K  I  C  E  L  S  A  M>    280
  A  T  P  V  P  A  H  P  A  S  T  A  K  S  V  N  *  V  P  *>   280
Q  L  L  L  Y  L  P  T  R  L  L  R  Q  N  L  *  I  E  C  H>     279

      850        860        870        880        890        900
       *    *     *    *     *    *     *    *     *    *     *    *
ACCTGTGCGG ACGGCCCTTG CTTTAACGGG GGTCGGTGCT CAGACAGCCC CGATGGAGGG
 T  C  A  D  G  P  C  F  N  G  G  R  C  S  D  S  P  D  G  G>    300
  P  V  R  T  A  L  A  L  T  G  V  G  A  Q  T  A  P  M  E  G>   300
D  L  C  G  R  P  L  L  *  R  G  S  V  L  R  Q  P  R  W  R>     299

      910        920        930        940        950        960
       *    *     *    *     *    *     *    *     *    *     *    *
TACAGCTGCC GCTGCCCCGT GGGCTACTCC GGCTTCAACT GTGAGAAGAA AATTGACTAC
 Y  S  C  R  C  P  V  G  Y  S  G  F  N  C  E  K  K  I  D  Y>    320
  T  A  A  A  A  P  W  A  T  P  A  S  T  V  R  R  K  L  T  T>   320
V  Q  L  P  L  P  R  G  L  L  R  L  Q  L  *  E  E  N  *  L>     319

      970        980        990       1000       1010       1020
       *    *     *    *     *    *     *    *     *    *     *    *
TGCAGCTCTT CACCCTGTTC TAATGGTGCC AAGTGTGTGG ACCTCGGTGA TGCCTACCTG
 C  S  S  S  P  C  S  N  G  A  K  C  V  D  L  G  D  A  Y  L>    340
  A  A  L  H  P  V  L  M  V  P  S  V  W  T  S  V  M  P  T  C>   340
L  Q  L  F  T  L  F  *  W  C  Q  V  C  G  P  R  *  C  L  P>     339

     1030       1040       1050       1060       1070       1080
       *    *     *    *     *    *     *    *     *    *     *    *
TGCCGCTGCC AGGCCGGCTT CTCGGGGAGG CACTGTGACG ACAACGTGGA CGACTGCGCC
 C  R  C  Q  A  G  F  S  G  R  H  C  D  D  N  V  D  D  C  A>    360
  A  A  A  R  P  A  S  R  G  G  T  V  T  T  T  W  T  T  A  P>   360
V  P  L  P  G  R  L  L  G  E  A  L  *  R  Q  R  G  R  L  R>     359
```

FIG.12B3

```
      1090      1100      1110      1120      1130      1140
        *    *    *    *    *    *    *    *    *    *    *    *
TCCTCCCCGT GCGCCAACGG GGGCACCTGC CGGGATGGCG TGAACGACTT CTCCTGCACC
 S  S  P   C  A  N  G   G  T  C   R  D  G   V  N  D  F   S  C  T>   380
  P  P  R   A  P  T   G  A  P  A   G  M  A   *  T  T   S  P  A  P>  380
L  L  P  V   R  Q  R   G  H  L   P  G  W  R   E  R  L   L  L  H>    379

      1150      1160      1170      1180      1190      1200
        *    *    *    *    *    *    *    *    *    *    *    *
TGCCCGCCTG GCTACACGGG CAGGAACTGC AGTGCCCCCG CCAGCAGGTG CGAGCACGCA
 C  P  P   G  Y  T  G   R  N  C   S  A  P   A  S  R  C   E  H  A>   400
  A  R  L   A  T  R   A  G  T  A   V  P  P   P  A  G   A  S  T  H>  400
L  P  A  W   L  H  G   Q  E  L   Q  C  P  R   Q  Q  V   R  A  R>    399

      1210      1220      1230      1240      1250      1260
        *    *    *    *    *    *    *    *    *    *    *    *
CCCTGCCACA ATGGGGCCAC CTGCCACGAG AGGGGCCACC GCTATNTGTG CGAGTGTGCC
 P  C  H   N  G  A  T   C  H  E   R  G  H   R  Y  X   C  E  C  A>   420
  P  A  T   M  G  P   P  A  T  R   G  A  T   A  I  C   A  S  V  P>  420
T  L  P  Q   W  G  H   L  P  R   E  G  P  P   L  F  V   R  V  C>    419

      1270      1280      1290      1300      1310      1320
        *    *    *    *    *    *    *    *    *    *    *    *
CGAAGCTACG GGGGTCCCAA CTGCCANTTC CTGCTCCCCG AAACTGCCCC CCCGGCCCCA
 R  S  Y   G  G  P  N   C  X  F   L  L  P   E  T  A  P   P  A  P>   440
  E  A  T   G  V  P   T  A  X  S   C  S  P   K  L  P   P  R  P  H>  440
P  K  L  R   G  S  Q   L  P  X   P  A  P  R   N  C  P   P  G  P>    439

      1330      1340      1350      1360      1370      1380
        *    *    *    *    *    *    *    *    *    *    *    *
CGGTGGTGGA AACTCCCCTA AAAAAACCTA AAAGGGCCGG GGGGGGCCCA TCCCCTTGGT
 R  W  W   K  L  P  *   K  N  L   K  G  P   G  G  A  H   P  L  G>   460
  G  G  G   N  S  P   K  K  T  *   K  G  R   G  G  P   I  P  L  V>  460
T  V  V  E   T  P  L   K  K  P   K  R  A  G   G  G  P   S  P  W>    459

      1390      1400      1410      1420      1430      1440
        *    *    *    *    *    *    *    *    *    *    *    *
GGACGTGTGC GCCGGGGTCA TCCTTGTCCT CATGCTGCTG CTGGGCTGTC CCGCTGTGGT
 G  R  V   R  R  G  H   P  C  P   H  A  A   A  G  L  C   R  C  G>   480
  D  V  C   A  G  V   I  L  V  L   M  L  L   L  G  C   A  A  V  V>  480
W  T  C  A   P  G  S   S  L  S   S  C  C  C   W  A  V   P  L  W>    479
```

FIG.12B4

```
       1450      1460      1470      1480      1490      1500
         *    *    *    *    *    *    *    *    *    *    *    *
GGTCTGCGTC CGGCTGAGGC TGCAGAAGCA CCGGCCCCCA GCCGACCCCT GNCGGGGGGA
 G  L  R  P  A  E  A  A  E  A  P  A  P  S  R  P  L  X  G  C>  500
 V  C  V  R  L  R  L  Q  K  H  R  P  P  A  D  P  X  R  G  E>  500
W  S  A  S  G  *  G  C  R  S  T  G  P  Q  P  T  P  X  G  G>   499

       1510      1520      1530      1540      1550      1560
         *    *    *    *    *    *    *    *    *    *    *    *
GACGGAGACC ATGAACAACC TGGNCAACTG CCAGCGTGAG AAGGACATCT CAGTCAGCAT
 D  C  D  H  E  Q  P  G  Q  L  P  A  *  E  G  H  L  S  Q  H>  520
 T  E  T  M  N  N  L  X  N  C  Q  R  E  K  D  I  S  V  S  I>  520
R  R  R  P  *  T  T  W  X  T  A  S  V  R  R  T  S  Q  S  A>   519

       1570      1580      1590      1600      1610      1620
         *    *    *    *    *    *    *    *    *    *    *    *
CATCGGGGNC ACGCAGATCA AGAACACCAA CAAGAAGGCG GACTTCCACG GGGACCACAG
 H  R  G  H  A  D  Q  E  H  Q  Q  E  G  G  L  P  R  G  P  Q>  540
 I  G  X  T  Q  I  K  N  T  N  K  K  A  D  F  H  G  D  H  X>  540
S  S  G  X  R  R  S  R  T  P  T  R  R  R  T  S  T  G  T  T>   539

       1630      1640      1650      1660      1670      1680
         *    *    *    *    *    *    *    *    *    *    *    *
NGCCGACAAG AATGGCTTCA AGGCCCGCTA CCCAGNGGTG GACTATAACC TCGTGCAGGA
 X  R  Q  E  W  L  Q  G  P  L  P  X  G  G  L  *  P  R  A  G>  560
 A  D  K  N  G  F  K  A  R  Y  P  X  V  D  Y  N  L  V  Q  D>  560
X  P  T  R  M  A  S  R  P  A  T  Q  X  W  T  I  T  S  C  R>   559

       1690      1700      1710      1720      1730      1740
         *    *    *    *    *    *    *    *    *    *    *    *
CCTCAAGGGT GACGACACCG CCGTCAGGGA CGCGCACAGC AAGCGTGACA CCAAGTGNCA
 P  Q  G  *  R  H  R  R  Q  G  R  A  Q  Q  A  *  H  Q  V  X>  580
 L  K  G  D  D  T  A  V  R  D  A  H  S  K  R  D  T  K  X  Q>  580
T  S  R  V  T  T  P  P  S  G  T  R  T  A  S  V  T  P  S  X>   579

       1750      1760      1770      1780      1790      1800
         *    *    *    *    *    *    *    *    *    *    *    *
GCCCCAGGGC TCCTCAGGGG AGGAGAAGGG GACCCCCGAC CCACACTCAG GGGGTGGAGG
 A  P  G  L  L  R  G  G  E  G  D  P  R  P  T  L  R  G  W  R>  600
 P  Q  G  S  S  G  E  E  K  G  T  P  D  P  H  S  G  G  G  G>  600
S  P  R  A  P  Q  G  R  R  R  G  P  P  T  H  T  Q  G  V  E>   599
```

FIG.12B5

```
        1810      1820      1830      1840      1850      1860
           *         *         *         *         *         *         *         *         *         *         *         *
AAGCATCTTG AAAGAAAAAG GCCGGACTTC GGGCTTGTTC AACTTTCAAA AGACAANCAA
 K  H  L   E  R  K  R  P  D  F   G  L  V   Q  L  S  K  D  X  Q>   620
  S  I  L   K  E  K  G  R  T  S   G  L  F   N  F  Q  K  T  X  X>  620
E  A  S  *  K  K  K  A  G  L   R  A  C  S  T  F  K  R  Q  X>     619

        1870      1880      1890      1900      1910      1920
           *         *         *         *         *         *         *         *         *         *         *         *
NGTACAAGTC GGTGTNCGTC ATTTCCGNAG GAGGAAGGNT GACTGCGTCA TAGGAANTTG
 X  T  S   R  C  X  S   F  P  X   E  E  G  *  L  R  H   R  X  L>  640
  V  Q  V   G  V  R   H  F  R  R   R  K  X   D  C  V  I  G  X  *>  640
X  Y  K  S   V  X  V   I  S  X   G  G  R  X   T  A  S   *  E  X>  639

        1930      1940      1950      1960      1970      1980
           *         *         *         *         *         *         *         *         *         *         *         *
AGGTNGTAAA NTGGNAGTTG ANNTTGGAAA GNNNTCCCCC GATTCCCNTT TCAAAGTTTT
 R  X  *   X  G  S  *   X  W  K   X  X  P   G  F  R  F   Q  S  F>  660
  G  X  K   X  X  V   X  X  G  K   X  S  P   D  S  X   F  K  V  F>  660
E  V  V  X   W  X  L   X  L  E   X  X  P  R   I   P  X  S  K  F>  659
```

FIG.12B6

```
MOUSE DELTA DNA   GTCCAGCGGT ACCATGGGCC GTCGGAGCGC GCTAGCCCTT GCCGTGGTCT   50
HUMAN DELTA       ---------- ---------- ---------- ---------- ----------

CONSENSUS         GTCCAGCGGT ACCATGGGCC GTCGGAGCGC GCTAGCCCTT GCCGTGGTCT   50

MOUSE DELTA DNA   CTGCCCTGCT GTGCCAGGTC TGGAGCTCCG GCGTATTTGA GCTGAAGCTG  100
HUMAN DELTA       ---------- ---------- ---------- ---------- ----------

CONSENSUS         CTGCCCTGCT GTGCCAGGTC TGGAGCTCCG GCGTATTTGA GCTGAAGCTG  100

MOUSE DELTA DNA   CAGGAGTTCG TCAACAAGAA GGGGCTGCTG GGGAACCGCA ACTGCTGCCG  150
HUMAN DELTA       ---------- ---------- ---------- ---------- ----------

CONSENSUS         CAGGAGTTCG TCAACAAGAA GGGGCTGCTG GGGAACCGCA ACTGCTGCCG  150

MOUSE DELTA DNA   CGGGGGCTCT GGCCCGCCTT GCGCCTGCAG GACCTTCTTT CGCGTATGCC  200
HUMAN DELTA       ---------- ---------- ---------- ---------- ----------

CONSENSUS         CGGGGGCTCT GGCCCGCCTT GCGCCTGCAG GACCTTCTTT CGCGTATGCC  200

MOUSE DELTA DNA   TCAAGCACTA CCAGGCCAGC GTGTCACCGG AGCCACCCTG CACCTACGGC  250
HUMAN DELTA       ---------- ---------- ---------- ---------- ----------

CONSENSUS         TCAAGCACTA CCAGGCCAGC GTGTCACCGG AGCCACCCTG CACCTACGGC  250

MOUSE DELTA DNA   AGTGCTGTCA CGCCAGTGCT GGGTGTCGAC TCCTTCAGCC TGCCTGATGG  300
HUMAN DELTA       ---------- ---------- ---------- ---------- -----CATTG    5

CONSENSUS         AGTGCTGTCA CGCCAGTGCT GGGTGTCGAC TCCTTCAGCC TGCCTSATKG  300

MOUSE DELTA DNA   CGCAGGCATC GACCCC---G CCTTCAGCAA CCCCA--TCC GAT-TC-CCC  343
HUMAN DELTA       GGTACGGGCC CCCCTCGAGG TCGACGGTAT CGATAAGCTT GATATCGAAT   55

CONSENSUS         SGYASGSRYC SMCCYCGAGG YCKWCRGYAW CSMYAAGYYY GATATCGMMY  350

MOUSE DELTA DNA   TTCGGCTTCA CCTGGCCAGG TACCTTCTCT CTGATCATTG AAGCCCTCCA  393
HUMAN DELTA       TCCGGCTTCA CCTGGCCGGG CACCTTCTCT CTGATTATTG AAGCTCTCCA  105

CONSENSUS         TYCGGCTTCA CCTGGCCRGG YACCTTCTCT CTGATYATTG AAGCYCTCCA  400

MOUSE DELTA DNA   TACAGACTCT CCCGATGACC TCGCAACAGA AAACCCAGAA AGACTCATCA  443
HUMAN DELTA       CACAGATTCT CCTGATGACC TCGCAACAGA AAACCCAGAA AGACTCATCA  155

CONSENSUS         YACAGAYTCT CCYGATGACC TCGCAACAGA AAACCCAGAA AGACTCATCA  450
```

FIG.13A

```
MOUSE DELTA DNA  GCCGCCTGAC CACACAGAGG CACCTCACTG TGGGAGAAGA ATGGTCTCAG  493
HUMAN DELTA      GCCGCCTGGC CACCCAGAGG CACCTGACGG TGGGCGAGGA GTGGTCCCAG  205

CONSENSUS        GCCGCCTGRC CACMCAGAGG CACCTSACKG TGGGMGARGA RTGGTCYCAG  500

MOUSE DELTA DNA  GACCTTCACA GTAGCGGCCG CACAGACCTC CGGTACTCTT ACCGCTTTGT  543
HUMAN DELTA      GACCTGCACA GCAGCGGCCG CACGGACCTC AAGTACTCCT ACCGCTTCGT  255

CONSENSUS        GACCTKCACA GYAGCGGCCG CACRGACCTC MRGTACTCYT ACCGSTTYGT  550

MOUSE DELTA DNA  GTGTGACGAG CACTACTACG GAGAAGGTTG CTCTGTCTTC TGCCGACCTC  593
HUMAN DELTA      GTGTGACGAA CACTACTACG GAGAGGGCTG CTCCGTTTTC TGCCGTCCCC  305

CONSENSUS        GTGTGACGAR CACTACTACG GAGARGGYTG CTCYGTKTTC TGCCGWCCYC  600

MOUSE DELTA DNA  GGGATGACGC CTTTGGCCAC TTCACCTGCG GGGACAGAGG GGAGAAGATG  643
HUMAN DELTA      GGGACGATGC CTTCGGCCAC TTCACCTGTG GGGAGCGTGG GGAGAAAGTG  355

CONSENSUS        GGGAYGAYGC CTTYGGCCAC TTCACCTGYG GGGASMGWGG GGAGAARRTG  650

MOUSE DELTA DNA  TGCGACCCTG GCTGGAAAGG CCAGTACTGC GCTGACCCAA TCTGTCTGCC  693
HUMAN DELTA      TGCAACCCTG GCTGGAAAGG GCCCTACTGC ACAGAGCCGA TCTGCCTGCC  405

CONSENSUS        TGCRACCCTG GCTGGAAAGG SCMSTACTGC ACWGASCCRA TCTGYCTGCC  700

MOUSE DELTA DNA  AGGCTGTGAT GACCAACATG GATACTGTGA CAAACCAGGG GAGTGCAAGT  743
HUMAN DELTA      TGGATGTGAT GAGCAGCATG GATTTTGTGA CAAACCAGGG GAATGCAAGT  455

CONSENSUS        WGGRTGTGAT GASCARCATG GATWYTGTGA CAAACCAGGG GARTGCAAGT  750

MOUSE DELTA DNA  GCAGAGTTGG CTGGCAGGGC CGCTACTGCC ATGAGTGCAT CCGATACCCA  793
HUMAN DELTA      GCAGAGTGGG CTGGCAGGGC CGITACTGTG ACGAGTGTAT CCGCTATCCA  505

CONSENSUS        GCAGAGTKGG CTGGCAGGGC CGSTACTGYS AYGAGTGYAT CCGMTAYCCA  800

MOUSE DELTA DNA  GGTTGTCTCC ATGGCACCTG CCAGCAACCC TGGCAGTGTA ACTGCCAGGA  843
HUMAN DELTA      GGCTGTCTCC ATGGCACCTG CCAGCAGCCC TGGCAGTGCA ACTGCCAGGA  555

CONSENSUS        GGYTGTCTCC ATGGCACCTG CCAGCARCCC TGGCAGTGYA ACTGCCAGGA  850

MOUSE DELTA DNA  AGGCTGGGGG GGCCTTTTCT GCAACCAAGA CCTGAACTAC TGTACTCACC  893
HUMAN DELTA      AGGNTGGGGG GGCCTTTTCT GCAACCAGGA CCTGAACTAC TGCACACACC  605

CONSENSUS        AGGNTGGGGG GGCCTTTTCT GCAACCARGA CCTGAACTAC TGYACWCACC  900
```

FIG.13B

MOUSE DELTA DNA ATAAGCCGTG CAGGAATGGA GCCACCTGCA -CCAACACGG GCCAGGGG-A 941
HUMAN DELTA ATAAGCCCTG CAAGAATGGA GCCACCTGCA ACAAACACGG GCCAGGGGGA 655
CONSENSUS ATAAGCCSTG CARGAATGGA GCCACCTGCA ACMAACACGG GCCAGGGGGA 950

MOUSE DELTA DNA GCTACACATG TTCCT--GCC -GACCTGGGT ATACA-GGTG CCAACTGTG- 986
HUMAN DELTA GCTACACTTG GTCTTTGGCC CGNCTGGGGT ACANAGGGTG CCACCTGCGA 705
CONSENSUS GCTACACWTG KTCYTTGGCC CGNCYKGGGT AYANAGGGTG CCAMCTGYGA 1000

MOUSE DELTA DNA AGCT--GGAA GTAGATGAG- TG-TGCTCCT AGCCCCT-GC AAGAACGGAG 1031
HUMAN DELTA AGCTTGGGGA TTGGACGAGT TGTTGACCCC AGCCCTTGGT AAGAACGGAG 755
CONSENSUS AGCTTGGGRA KTRGAYGAGT TGTTGMYCCY AGCCCYTGGY AAGAACGGAG 1050

MOUSE DELTA DNA CGAGCTGCAC GGACCTT--G AGGACAGCTT CTCTTGCACC TGCCCTCCCG 1079
HUMAN DELTA GGAGCTTGAC GGATCTTCGG AGAACAGCTA CTCCTGTACC TGCCCACCCG 805
CONSENSUS SGAGCTKSAC GGAYCTTCGG AGRACAGCTW CTCYTGYACC TGCCCWCCCG 1100

MOUSE DELTA DNA GCTTCTATGG CAAGGTCTGT GAGCTGAGCG CCATGACCTG TGCAGATGGC 1129
HUMAN DELTA GCTTCAACGG CAAAATCTGT GAATTGAGTG CCATGACCTG TGCGGACGGC 855
CONSENSUS GCTTCTAYGG CAARRTCTGT GARYTGAGYG CCATGACCTG TGCRGAYGGC 1150

MOUSE DELTA DNA CCTTGCTTCA ATGGAGGACG ATGTTCAGAT AACCCTGACG GAGGCTACAC 1179
HUMAN DELTA CCTTGCTTTA ACGGCGGTCG GTGCTCAGAC AGCCCCGATG GAGGGTACAG 905
CONSENSUS CCTTGCTTYA AYGGRGGWCG RTGYTCAGAY ARCCCYGAYG GAGGSTACAS 1200

MOUSE DELTA DNA CTGCCATTGC CCCTTGGGCT TCTCTGGCTT CAACTGTGAG AAGAAGATGG 1229
HUMAN DELTA CTGCCGCTGC CCCGTGGGCT ACTCCGGCTT CAACTGTGAG AAGAAAATTG 955
CONSENSUS CTGCCRYTGC CCCKTGGGCT WCTCYGGCTT CAACTGTGAG AAGAARATKG 1250

MOUSE DELTA DNA ATCTCTGCGG CTCTTCCCCT TGTTCTAACG GTGCCAAGTG TGTGGACCTC 1279
HUMAN DELTA ACTACTGCAG CTCTTCACCC TGTTCTAATG GTGCCAAGTG TGTGGACCTC 1005
CONSENSUS AYYWCTGCRG CTCTTCMCCY TGTTCTAAYG GTGCCAAGTG TGTGGACCTC 1300

MOUSE DELTA DNA GGCAACTCTT ACCTGTGCCG CTGCCAGGCT GGCTTCTCCG GGAGGTACTG 1329
HUMAN DELTA GGTGATGCCT ACCTGTGCCG CTGCCAGGCC GGCTTCTCGG GGAGGCACTG 1055
CONSENSUS GGYRAYKCYT ACCTGTGCCG CTGCCAGGCY GGCTTCTCSG GGAGGYACTG 1350

MOUSE DELTA DNA CGAGGACAAT GTGGATGACT GTGCCTCCTC CCCGTGTGCA AATGGGGGCA 1379
HUMAN DELTA TGACGACAAC GTGGACGACT GCGCCTCCTC CCCGTGCGCC AACGGGGGCA 1105
CONSENSUS YGASGACAAY GTGGAYGACY GYGCCTCCTC CCCGTGYGCM AAYGGGGGCA 1400

FIG. 13C

| | | |
|---|---|---|
| MOUSE DELTA DNA | CCTGCCGGGA CAGTGTGAAC GACTTCTCCT GTACCTGCCC ACCTGGCTAC | 1429 |
| HUMAN DELTA | CCTGCCGGGA TGGCGTGAAC GACTTCTCCT GCACCTGCCC GCCTGGCTAC | 1155 |
| CONSENSUS | CCTGCCGGGA YRGYGTGAAC GACTTGTCCT GYACCTGCCC RCCYGGCTAC | 1450 |
| MOUSE DELTA DNA | ACGGGCAAGA ACTGCAGCGC CCCTGTCAGC AGGTCTGAGC ATGCACCCTG | 1479 |
| HUMAN DELTA | ACGGGCAGGA ACTGCAGTGC CCCCGCCAGC AGGTCCGAGC ACGCACCCTG | 1205 |
| CONSENSUS | ACGGGCARGA ACTGCAGYGC CCCYGYCAGC AGGTCYGAGC AYGCACCCTG | 1500 |
| MOUSE DELTA DNA | CCATAATGGG GCCACCTGCC ACCAGAGGGG CCAGCGCTAC ATGTGTGAGT | 1529 |
| HUMAN DELTA | CCACAATGGG GCCACCTGCC ACGAGAGGGG CCACCGCTAT TTGTGCGAGT | 1255 |
| CONSENSUS | CCAYAATGGG GCCACCTGCC ACSAGAGGGG CCASCGCTAY WTGTGYGAGT | 1550 |
| MOUSE DELTA DNA | GCGCCCAGGG CTATGGCGGC CCCAACTGCC AGTTTCTGCT CCCTG-AGCC | 1578 |
| HUMAN DELTA | GTGCCCGAAG CTACGGGGGT CCCAACTGCC ANTTCCTGCT CCCCGAAACT | 1305 |
| CONSENSUS | GYGCCCRRRG CTAYGGSGGY CCCAACTGCC ANTTYCTGCT CCCYGAARCY | 1600 |
| MOUSE DELTA DNA | -ACCACCAGG GCCCATGGTG GTGG-ACCTC AGTGAGAGGC ATAT-GGAGA | 1625 |
| HUMAN DELTA | GCCCCCCCGG CCCCACGGTG GTGGAAACTC CCCTAAAAAA ACCTAAAAGG | 1355 |
| CONSENSUS | GMCCMCCMGG SCCCAYGGTG GTGGAAMCTC MSYKARARRM AYMTARRAGR | 1650 |
| MOUSE DELTA DNA | GCCAGGGCGG GCCCTTCCCC TGGGTGGCCG TGTGTGCCGG GGTGGTGCTT | 1675 |
| HUMAN DELTA | GCCGGGGGGG GCCCATCCCC TTGGTGGACG TGTGCGCCGG GGTCATCCTT | 1405 |
| CONSENSUS | GCCRGGGSGG GCCCWTCCCC TKGGTGGMCG TGTGYGCCGG GGTSRTSCTT | 1700 |
| MOUSE DELTA DNA | GTCCTCCTGC TGCTGCTGGG CTGTGCTGCT GTGGTGGTCT GCGTCCGGCT | 1725 |
| HUMAN DELTA | GTCCTCATGC TGCTGCTGGG CTGTGCCGCT GTGGTGGTCT GCGTCCGGCT | 1455 |
| CONSENSUS | GTCCTCMTGC TGCTGCTGGG CTGTGCYGCT GTGGTGGTCT GCGTCCGGCT | 1750 |
| MOUSE DELTA DNA | GAAGCTACAG AAACACCAGC CTCCATCTGA ACCCTGTGGG GGAGAGACAG | 1775 |
| HUMAN DELTA | GAGGCTGCAG AAGCACCGGC CCCCATCCGA CCCCTGNCGG GGGGAGACGG | 1505 |
| CONSENSUS | GARGCTRCAG AARCACCRGC CYCCASCYGA MCCCTGNSGG GGRGAGACRG | 1800 |
| MOUSE DELTA DNA | AAACCATGAA CAACCTAGCC AATTGCCAGC GCGAGAAGGA CGTTTCTGTT | 1825 |
| HUMAN DELTA | AGACCATGAA CAACCTGGNC AACTGCCAGC GTGAGAAGGA CATCTCAGTC | 1555 |
| CONSENSUS | ARACCATGAA CAACCTRGNC AAYTGCCAGC GYGAGAAGGA CRTYTCWGTY | 1850 |

FIG. 13D

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MOUSE DELTA DNA  AGCATCATTG GGGCTACCCA GATCAAGAAC ACCAACAAGA AGGCGGACTT  1875
HUMAN DELTA      AGCATCATCG GGGNCACGCA GATCAAGAAC ACCAACAAGA AGGCGGACTT  1605

CONSENSUS        AGCATCATYG GGGNYACSCA GATCAAGAAC ACCAACAAGA AGGCGGACTT  1900

MOUSE DELTA DNA  TCACGGGGAC CATGGAGCCA AGAAGAGCAG CTTTAAGGTC CGATACCCCA  1925
HUMAN DELTA      CCACGGGGAC CACAGNGCCG ACAAGAATGG CTTCAAGGCC CGCTACCCAG  1655

CONSENSUS        YCACGGGGAC CAYRGNGCCR ASAAGARYRG CTTYAAGGYC CGMTACCCMR  1950

MOUSE DELTA DNA  CTGTGGACTA TAACCTCGTT CGAGACCTCA AGGGAGATGA AGCCACCGTC  1975
HUMAN DELTA      NGGTGGACTA TAACCTCGTG CAGGACCTCA AGGGTGACGA CACCGCCGTC  1705

CONSENSUS        NKGTGGACTA TAACCTCGTK CRRGACCTCA AGGGWGAYGA MRCCRCSGTC  2000

MOUSE DELTA DNA  AGGGATACAC ACAGCAAACG TGACACCAAG TGCCAGTCAC AGAGCTCTGC  2025
HUMAN DELTA      AGGGACGCGC ACAGCAAGCG TGACACCAAG TGNCAGCCCC AGGGCTCCTC  1755

CONSENSUS        AGGGAYRCRC ACAGCAAFCG TGACACCAAG TGNCAGYCMC AGRGCTCYKC  2050

MOUSE DELTA DNA  AGGAGAAGAG AA---GATCG CC--CCAACA CTTA-GGGGT GG-GG-AGAT  2067
HUMAN DELTA      AGGGGAGGAG AAGGGGACCC CCGACCCACA CTCAGGGGGT GGAGGAAGCA  1805

CONSENSUS        AGGRGARGAG AAGGGGAYCS CCGACCMACA CTYAGGGGGT GGAGGAAGMW  2100

MOUSE DELTA DNA  TCCTGACAGA AAAAGGCCAG AGTCT--GTC TACTCTAC-T TCAAAGGAC-  2113
HUMAN DELTA      TCTTGAAAGA AAAAGGCCGG ACTTCGGGCT TGTTCAACTT TCAAAAGACA  1855

CONSENSUS        TCYTGAMAGA AAAAGGCCRG ASTYYGGGYY TRYTCWACTT TCAAARGACA  2150

MOUSE DELTA DNA  -ACCAAGTAC CAGTCGGTGT ATGTTCTGTC TGCAGAA--A AGGATGAGTG  2160
HUMAN DELTA      ANCAANGTAC AAGTCGGTGT NCGTCATTTC CGNAGGAGGA AGGNTGACTG  1905

CONSENSUS        ANCMANGTAC MAGTCGGTGT NYGTYMTKTC YGNAGRAGGA AGGNTGASTG  2200

MOUSE DELTA DNA  TGTTATA-GC GACTGAGGT- GTAAGATGGA AGCGATGTGG CAAAATTCCC  2208
HUMAN DELTA      CGTCATAGGA ANTTGAGGTN GTAAANTGGN AG---T-TG- --ANNTT---  1945

CONSENSUS        YGTYATAGGM RNYTGAGCTN GTAARNTGGN AGCGATGTGG CAANNTTCCC  2250

MOUSE DELTA DNA  ATTTCTCTCA AATAAAATTC CAAGGATATA GCCCCGATGA ATGCTGCTGA  2258
HUMAN DELTA      -------GGA AAGNNN--TC CCCGGAT--- --TCCGNT-- ----TTC---  1972

CONSENSUS        ATTTCTCKSA AAKNNNATTC CMMGGATATA GCYCCGNTGA ATGCTKCTGA  2300
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FIG.13E

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MOUSE DELTA DNA GAGAGGAAGG GAGAGGAAAC CCAGGGACTG CTGCTGAGAA CCAGGTTCAG  2308
HUMAN DELTA     ---------- ------AAA- ---------G TTTTT----- ----------  1981

CONSENSUS       GAGAGGAAGG GAGAGGAAAC CCAGGGACTG YTKYTCAGAA CCAGGTTCAG  2350

MOUSE DELTA DNA GCGAAGCTGG TTCTCTCAGA GTTAGCAGAG GCGCCCGACA CTGCCAGCCT  2358
HUMAN DELTA     ---------- ---------- ---------- ---------- ----------  1981

CONSENSUS       GCGAAGCTGG TTCTCTCAGA GTTAGCAGAG GCGCCCGACA CTGCCAGCCT  2400

MOUSE DELTA DNA AGGCTTTGGC TGCCGCTGGA CTGCCTGCTG GTTGTTCCCA TTGCACTATG  2408
HUMAN DELTA     ---------- ---------- ---------- ---------- ----------  1981

CONSENSUS       AGGCTTTGGC TGCCGCTGGA CTGCCTGCTG GTTGTTCCCA TTGCACTATG  2450

MOUSE DELTA DNA GACAGTTGCT TTGAAGAGTA TATATTTAAA TGGACGAGTG ACTTGATTCA  2458
HUMAN DELTA     ---------- ---------- ---------- ---------- ----------  1981

CONSENSUS       GACAGTTGCT TTGAAGAGTA TATATTTAAA TGGACGAGTG ACTTGATTCA  2500

MOUSE DELTA DNA TATAGGAAGC ACGCACTGCC CACACGTCTA TCTTGGATTA CTATGAGCCA  2508
HUMAN DELTA     ---------- ---------- ---------- ---------- ----------  1981

CONSENSUS       TATAGGAAGC ACGCACTGCC CACACGTCTA TCTTGGATTA CTATGAGCCA  2550

MOUSE DELTA DNA GTCTTTCCTT GAACTAGAAA CACAACTGCC TTTATTGTCC TTTTTGATAC  2558
HUMAN DELTA     ---------- ---------- ---------- ---------- ----------  1981

CONSENSUS       GTCTTTCCTT GAACTAGAAA CACAACTGCC TTTATTGTCC TTTTTGATAC  2600

MOUSE DELTA DNA TGAGATGTGT TTTTTTTTTT CCTAGACGGG AAAAAGAAAA CGTGTGTTAT  2608
HUMAN DELTA     ---------- ---------- ---------- ---------- ----------  1981

CONSENSUS       TGAGATGTGT TTTTTTTTTT CCTAGACGGG AAAAAGAAAA CGTGTGTTAT  2650

MOUSE DELTA DNA TTTTTTGGGA TTTGTAAAAA TATTTTTCAT GATATCTGTA AAGCTTGAGT  2658
HUMAN DELTA     ---------- ---------- ---------- ---------- ----------  1981

CONSENSUS       TTTTTTGGGA TTTGTAAAAA TATTTTTCAT GATATCTGTA AAGCTTGAGT  2700

MOUSE DELTA DNA ATTTTGTGAC GTTCATTTTT TTATAATTTA AATTTTGGTA AATATGTACA  2708
HUMAN DELTA     ---------- ---------- ---------- ---------- ----------  1981

CONSENSUS       ATTTTGTGAC GTTCATTTTT TTATAATTTA AATTTTGGTA AATATGTACA  2750
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FIG.13F

| | | | | | | |
|---|---|---|---|---|---|---|
| MOUSE DELTA DNA | AAGGCACTTC | GGGTCTATGT | GACTATATTT | TTTTGTATAT | AAATGTATTT | 2758 |
| HUMAN DELTA | ---------- | ---------- | ---------- | ---------- | ---------- | 1981 |
| CONSENSUS | AAGGCACTTC | GGGTCTATGT | GACTATATTT | TTTTGTATAT | AAATGTATTT | 2800 |
| MOUSE DELTA DNA | ATGGAATATT | GTGCAAATGT | TATTTGAGTT | TTTTACTGTT | TTGTTAATGA | 2808 |
| HUMAN DELTA | ---------- | ---------- | ---------- | ---------- | ---------- | 1981 |
| CONSENSUS | ATGGAATATT | GTGCAAATGT | TATTTGAGTT | TTTTACTGTT | TTGTTAATGA | 2850 |
| MOUSE DELTA DNA | AGAAATTCAT | TTTAAAAATA | TTTTTCCAAA | ATAAATATAA | TGAACTACA | 2857 |
| HUMAN DELTA | ---------- | ---------- | ---------- | ---------- | ---------- | 1981 |
| CONSENSUS | AGAAATTCAT | TTTAAAAATA | TTTTTCCAAA | ATAAATATAA | TGAACTACA | 2899 |

FIG.13G

G F T W P G T F S L I I E A L H T D S P D> 21

D L A T E N P E R L I S R L A T Q R H L> 41

T V G E E W S Q D L H S S G R I D L K Y> 61

S Y R F V C D E H Y Y G E G C S V F C R> 81

P R D D A F G H F T C G E R G E K V C N> 101

P G W K G P Y C T E P I C L P G C D E Q> 121

H G F C D K P G E C K C R V G W Q G R Y> 141

C D E C I R Y P G C L H G T C Q Q P W Q> 161

C N C Q E G W G G L F C N Q D L N Y C T> 181

H H K P C K N G A T C * T N T G Q G * 198

S Y T * P S P * K N G G S L T D L * 213

E N S Y S C T C P P G F Y G K I C E L S A M> 235

T C A D G P C F N G G R C S D S P D G G> 255

Y S C R C P V G Y S G F N C E K K I D Y> 275

C S S S P C S N G A K C V D L G D A Y L> 295

C R C Q A G F S G R H C D D N V D D C A> 315

S S P C A N G G T C R D G V N D F S C T> 335

C P P G Y T G R N C S A P A S R C E H A> 355

P C H N G A T C H E R G H R Y * C E C A> 374

R S Y G G P N C * F L L P E * P P G P *> 391

V V * L L L G C A A V V V C V R L R L Q K H> 412

R P P A D P * R G E T E T M N N L *> 428

FIG. 14A

N C Q R E K D I S V S I I G * T Q I K N T N> 449

K K A D F H G D H * A D K N G F K A R Y P * 469

V D Y N L V Q D L K G D D T A V R D A H S K R D T K * 494

Q P Q G S S G E E K G T P * P T L R * G G * 514

I * R K R P * S * S T * S K D * T * 526

C V I * E V * 531

FIG. 14B